between chemical moieties of DNA and RNA, stark contrasts in counterion interactions occured. In the presence of either 0.1M Na+ or 0.1M K+, ion dynamics were not significantly altered for a given duplex. However, greater deviations were seen between duplexes of different helical forms. A final inquiry into the role of geometry leads us to conclude that helical geometry is responsible for a greater majority of cationic interactions and diffusive ion binding than can be explained exclusively by electrostatics resulting from chemical moieties alone.

420-Pos Board B220

Driving Denaturation: Nanoscale Thermal Transport As a Probe of DNA Melting

Michael Zwolak, Kirill Velizhanin, Chih-Chun Chien, Yonatan Dubi.

DNA denaturation has long been a subject of intense study due to its relationship to DNA transcription and its fundamental importance as a nonlinear, structural transition. Many aspects of this phenomenon, however, remain poorly understood. Existing models fit quite well with experimental results on the fraction of unbound base pairs versus temperature. Yet, these same models give incorrect results for other essential quantities, e.g., the predicted base pair fluctuation timescales - relevant to transcription - are orders of magnitude different from experimental ones. Here, we demonstrate that nanoscale thermal transport can serve as a sensitive probe of the underlying microscopic mechanisms responsible for dynamics of DNA denaturation. Specifically, we show that the heat transport properties of DNA are altered significantly and abruptly as it denaturates, and this alteration encodes detailed information on the dynamics of thermal fluctuations and their interaction along the chain. This finding allows for the unambiguous discrimination between models of DNA denaturation. Measuring the thermal conductance will thus shed new light on the nonlinear physics of this important molecule. Furthermore, our observation of the surprisingly abrupt alteration of DNA heat conductance upon denaturation may lead to novel thermal technologies on nanoscale. In particular, we propose DNA as the working body of a thermal switch, whose properties can be switched between heat conducting and heat insulating under temperature control.

421-Pos Board B221

Electroperturbation of DNA in Jurkat Cells Under Nanosecond Pulsed Electric Fields

Stefania Romeo, Olga Zeni, Maria Rosaria Scarfi, Maurizio Sarti, Anna Sannino, **P Thomas Vernier**, Luigi Zeni.

Intense (5-30 MV/m) ultra-short (10-300 ns) pulsed electric fields (US-PEFs) have been demonstrated to interact with sub-cellular membranes and structures [*Schoenbach et al., IEEE Trans. Diel. El. Ins., 14 (5): 1088-1109, 2007*]. Investigating how cells respond to nanosecond pulses is essential for a) development of biomedical applications of US-PEFs, including cancer treatment, and b) better understanding of the mechanisms underlying such bioelectrical effects. T-lymphoblast Jurkat cells were exposed to a single pulse of 60 ns duration and 2.5 MV/m amplitude, without affecting cell growth and viability, to give insight into effects underlying interaction mechanisms. A cuvette-based exposure system, fed by a classical Blumlein pulse-forming network, was employed. A statistically significant reduction in DNA migration was detected immediately after US-PEF exposure by means of the alkaline comet assay [*Zeni et al., Sensors, 8: 485-496, 2008*]. This effect, associated with plasma membrane poration (YO-PRO-1 uptake) has been demonstrated to recover within 2 hours after pulse delivery (Figure 1), indicating that our exposure protocol targets the nucleus, affecting DNA structure. In our experimental conditions, a transient conformational change in DNA molecule can thus be hypothesized.

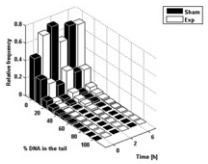

Figure 1: Effects on DNA migration in Jurkat cells exposed to single pulse (60 ns, 2.5 MV/m). Results are presented as distribution of % DNA in the comet tail for a representative experiment.

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Structure and Dynamics of the Bacterial Chromosome in E. coli

Nastaran Hadizadeh, Calin Guet, Reid C. Johnson, John F. Marko.

The bacterial cell's ability to control the topology of a long DNA in the confined environment of the cell is quite remarkable. Despite a great number of studies on bacteria, and especially E coli, our understanding of the spatio-temporal organization of bacterial chromosomes is minimal, partly because their dynamics have been difficult to observe directly. To visualize bacterial chromosome conformation within living cells, we have developed a bacterial strain containing fluorescent gfp-fusion versions of a chromosome folding protein, Fis, under inducible control. Bacterial chromosomes have been studied in cells and removed from cells, in order to establish their spatial organization and mechanical properties, and to study how those properties are changed by varied external conditions. Space-time studies of the nucleoid in live E coli cells shows a relation between chromosome segregation and cell division under different growth conditions, and it also shows how domain structure and overall conformation of chromosomes vary during rapid and slow growth. In order to study the bacterial chromosome outside of the cell, we have developed methods for isolation of single bacterial chromosomes and directly examining nucleoid mechanical properties as a function of protein levels using micromanipulation methods.

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Molecular Dynamics Simulation Studies on the Hybridization Events of Surface Immobilized DNA

Abhishek Singh, Yaroslava G. Yingling.

Surfaces functionalized with ssDNAs can be used to uniquely and reversibly bind complimentary DNAs. Such DNA modified materials are used in nanoscale supramolecular assembly, as optical, electrochemical and piezoelectric biosensors. Recognition and recombination pathways of DNA functionalized system are regulated by ssDNA hybridization. We conducted molecular dynamics simulation studies of DNA strands thiolated on the surface and in the presence of duplex and compared their dynamics to the dynamics of the DNA strands in solution. We investigated the optimal ssDNA length, effect of linker type and length to understand the effect of immobilization on subsequent DNA hybridization. Our results indicate that sensitivity and selectivity are directly dependent on the length and sequence of ssDNA strands. The persistence length, folding pathway and time are directly dependent on the hybridization and length of ssDNA. Minimum energy pathways were explored to understand the kinetics of ssDNA folding during the event of hybridization. Simulations suggest that restrained ssDNAs, compared to labile suspensions of free ssDNAs, are more capable of hybridization and hence DNA-based assembly. Our study helps understanding the science associated with the ssDNA hybridization and provides feedback to the associated experiments.

424-Pos Board B224

Infectious Disease-Based (tuberculosis, Malaria, and Aids) Alternative, Plasmid and Helical Transitional Nucleic Acid Microarrays: Next Generation of DNA Microarrays

Claude E. Gagna, Robert Dannibale, Kayvan D. Beheshti, Akaz John, Goretti Chiang, Shanacy Marler, Priya Nanda, Sarah Syed, Sahil Kohli, Shehryar Malik, Sabreen Rahman, Aney Patel, Job Joy, W. Clark Lambert.

Millions die every year from infectious diseases such as tuberculosis, malaria and AIDS. More research needs to be performed to find new target sites (exotic DNA) for treatments of these pathologies. The majority of DNA is right-handed double-stranded (ds-) B-DNA. However, other forms of nucleic acids exist, viz., ds-Z-DNA, triple-stranded DNA and four-stranded DNA. Our group has developed novel ds-DNA microarrays that contain tuberculosis genes (Mycobacterium tuberculosis) and malaria genes [i.e., Plasmodium falciparum (var, rif and stevor genes)]. Employing the novel microarrays allows for the entire genes or segments to be immobilized as intact, unaltered, nondenatured DNA molecules. These microarrays allow for the discovery of drugs that bind to the immobilized intact genes under different environmental conditions (with or without proteins, supercoiling, ionic conditions, drugs). They also allow characterization of DNA structure and function. Using the new microarrays and bioinformatics, genes can be characterized for the presence of B-DNA and Z-DNA (transcription studies). Genes that contain DNA with the potential for B-DNA to Z-DNA transitions can be studied under specific environmental conditions. These infectious disease-based microarrays will include ds-Z-DNA, ds-B-DNA, B-DNA/Z-DNA junctions, mitochondrial DNA, and helical transitional arrays (B-DNA to Z-DNA). These new microarrays will allow for unprecedented drug discovery and gene expression studies. They will go beyond the limitations of commercially available, conventional ss-DNA microarrays (hybridization), which only focus on DNA primary structure (base pairs) and ignore DNA secondary structure. With these new microarrays, researchers will have access to all of the previously unexplored DNA structures that regulate gene expression.